SEQUENCE LISTING

<110> Nakamura, Yusuke
      Furukawa, Yoichi

<120> METHOD FOR DIAGNOSING COLORECTAL CANCERS

<130> 082368-008900US

<150> PCT/JP2004/002145
<151> 2004-02-24

<160> 23

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tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg   296
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag   344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
                5   10   15

cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa   392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
            20   25   30

att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga   440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
        35   40   45

aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc   488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
    50   55   60   65

ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac   536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
                70   75   80

aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act   584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
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acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg   632

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Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
        115                 120                 125

caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa    728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys
130                 135                 140                 145

acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac    776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
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Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
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Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
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tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg    920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
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gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca    968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
210                 215                 220                 225

gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg    1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
                230                 235                 240

gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag    1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
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ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa    1112
Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr Gln
            260                 265                 270

aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca    1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
        275                 280                 285

gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa    1208
Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile Gln
290                 295                 300                 305

aaa ctc agg gaa gag aat gat att gct agg gga aaa ctt gaa gaa gag    1256
Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu Glu
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aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca    1304
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caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac   1400
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cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga   1448
Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
370             375             380                 385

aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat   1496
Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu His
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gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa   1544
Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
            405             410             415

aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc   1592
Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
        420             425             430

aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc   1640
Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
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act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag   1688
Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys  *
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        35                  40                  45
Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
    50                  55                  60
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Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65              70              75                      80
Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85              90                      95
Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
            100             105             110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
        115             120             125
Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
    130             135             140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145             150             155             160
Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
            165             170             175
Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
        180             185             190
Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
    195             200             205
Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
    210             215             220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225             230             235             240
Leu Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr
            245             250             255
Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
            260             265             270
Gln Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg
    275             280             285
Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
    290             295             300
Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305             310             315             320
Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
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Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
            340             345             350
Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
    355             360             365
Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
    370             375             380
Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385             390             395             400
His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
            405             410             415
Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
        420             425             430
Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
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9

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